IAPSAP/MPSA 2004 Pehr Edman and Young Investigator Awards - May 21, 2004

The 2004 IAPSAP/MPSA Pehr Edman Award will be presented to Dr. Stephen Altschul, Computational Biology Branch, National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health, USA, and to Dr. Amos Bairoch, Swiss Institute for Bioinformatics, Geneva, Switzerland.

Dr. Altschul received his AB from Harvard College in 1979 and his Ph.D. from the Massachusetts Institute of Technology in 1987. He has made many contributions to the field of protein sequence comparison and analysis. He is perhaps best known for his role in developing the BLAST and PSI_BLAST sequence database search programs. PSI_BLAST introduced rapid and fully automated iterated protein profile analysis to database searching. It has become a vital tool for genome annotation and for protein structure prediction and modeling studies. Dr. Altschul's other research activities include the description of statistics for local sequence alignments and SAGE analysis, the elucidation of the properties of amino acid substitution matrices, the development of the MSA, MACAW and Gibbs sampling algorithms for multiple sequence alignment, and the first description of the BRCT domain in BRCA1 and other DNA damage response proteins. For additional information, see http://www.ncbi.nlm.nih.gov/CBBresearch/Altschul/.

Dr. Bairoch received his Masters of Science in Biochemistry from the University of Geneva in 1983 and his Ph.D. in 1990. His main efforts have been in the field of protein sequence analysis and the development of databases and software tools for the analysis of proteins. He is best known for the development and maintenance of the Swiss-Prot database, the best known and most widely used database on proteins. From 1987 to 1994 Swiss-Prot was a collaborative project with the European Molecular Biology Laboratory and since 1994 with the European Bioinformatics Institute (EBI). Dr. Bairoch has also developed PROSITE, a database of protein families and domains, ENZYME, a database of information on the nomenclature of enzymes, and contributed to the development of ExPASy, a web server for molecular biologists. Currently he is Professor of Bioinformatics in the Department of Structural Biology and Bioinformatics at the University of Geneva. For additional information, see: http://www.expasy.org/people/personal/amos/amos_home.html

The Pehr Edman Award is given to individuals whose efforts have significantly advanced the fields of protein chemistry, protein structure analysis, or proteomics. The award honors and commemorates the work of Pehr Edman, the Swedish chemist principally responsible for developing the chemistry for sequencing proteins by removing amino acids from the amino terminus one at a time. The Award is given in conjunction with Methods in Protein Structure Analysis (MPSA) meetings, which are sponsored by the International Association for Protein Structure Analysis and Proteomics (www.iapsap.bnl.gov). The first prize was awarded to Richard Laursen in 1988 for his efforts in the development of solid-state protein sequencing methods. In 2002, the award was given to Professor Hans Jörnvall, Karolinska Institute, Stockholm, Sweden, for contributions to protein chemistry, structure and function through the development of techniques associated with the use of Edman chemistry and structure-function studies on alcohol dehydrogenases, and to Professor Kenneth Walsh, University of Washington, Seattle, Washington, USA for his contributions to the development of mass spectrometry for characterizing the chemical structure of proteins and their posttranslational modifications and for concepts contributing to the evolution of protein structure and function.

The 2004 Pehr Edman Awards are supported by Applied Biosystems, Inc. and will be presented at MPSA2004 (http://depts.washington.edu/biowww/mpsa2004), which will take place August 29 through September 2, 2004 on the campus of the University of Washington, Seattle, WA.

The 2002 IAPSAP/MPSA Young Investigator Award, supported by Applied Biosystems, Inc., will be given to Dr. Niroshan Ramachandran, Harvard Institute of Proteomics, Department of Biological Chemistry and Molecular Pharmacology, Harvard University, Boston, MA 02115, USA

Dr. Ramachandran, currently a postdoctoral fellow in Dr. Joshua LaBaer's lab, has developed a novel self -assembling protein microarray. In this approach, Nucleic Acid Programmable Protein Array (NAPPA), proteins self assemble from nucleic acids. Traditional target protein microarrays are generated by expressing, purifying and spotting the proteins on a microarray. Dr. Ramachandran's approach begins with spotting full-length cDNAs, which are then transcribed and translated using a eukaryotic cell-free expression system. This approach offers a number of advantages over conventional protein microarrays: first, it eliminates the need for tedious and laborious methods for protein purification; second, it reduces concerns about protein stability as the proteins are produced just-in-time; lastly, it allows expression of mammalian proteins in a mammalian milieu that contains the necessary machinery to ensure the integrity of mammalian proteins. Dr. Ramachandran has used this technology to build a protein interaction network among human DNA replication proteins, to study regulation of protein interaction and to map binding domains. He currently is building a microarray expressing the 1000 most relevant genes in breast cancer (BC1000 gene collection - FLEXGene repository). The BC1000 microarray will be used to interrogate the functions of these genes and to develop diagnostic tools for breast cancer.

Dr. Ramachandran will receive his award this fall at MPSA2004 in Seattle, WA. IAPSAP created the Young Investigator Award in 2000 to recognize promising young investigators who are beginning to advance the fields of protein chemistry, protein structure analysis, or proteomics. The first award was given Dr. Kristian Müller, now in Freiburg, Germany; the 2002 Young Investigator award was presented to Dr. Dorothee Kern, Brandeis University at MPSA2002 in Valencia, Spain.